



CLAIMS

What is claimed is:

- 1. A genetic vector for stable transfection and expression of a desired protein within eukaryotic cells comprising:
 - (a) distal 5' flanking sequences of a eukaryotic locus;
 - (b) proximal 5' regulatory sequences of a eukaryotic locus;
 - (c) at least a first insertion site for a first heterologous coding sequence; and
- (d) proximal 3' regulatory sequences effective for transcription termination of a eukaryotic locus;

wherein said sequences are operably joined in order (a)-(d) in a 5' to 3' orientation, with optional linker sequences between adjacent sequences; and wherein

- (1) said distal 5' flanking sequences comprise a sequence of at least 100 bases

 having at least 70% identity to a nucleotide sequence found between 20 bp and 100,000

 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus; or
 - (2) said proximal 5' regulatory sequences comprise a sequence of at least 20 bases having at least 70% identity to a nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

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- 2. A genetic vector for stable transfection and expression of a desired protein within eukaryotic cells comprising:
 - (a) distal 5' flanking sequences of a eukaryotic locus;
 - (b) proximal 5' regulatory sequences of a eukaryotic locus;
- 25 (c) at least a first heterologous coding sequence encoding said desired protein; and
 - (d) proximal 3' regulatory sequences effective for transcription termination of a eukaryotic locus;

wherein said sequences are operably joined in order (a)-(d) in a 5' to 3'
orientation, with optional linker sequences between adjacent sequences; and
wherein

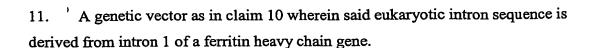
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- (1) said distal 5' flanking sequences comprise a sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus; or
- (2) said proximal 5' regulatory sequences comprise a sequence of at least 20 bases having at least 70% identity to a nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.
 - 3. A genetic vector as in any one of claims 1-2 wherein said distal 5' flanking sequences are derived from a ferritin heavy chain locus.
 - 4. A genetic vector as in any one of claims 1-2 wherein said proximal 5' regulatory sequences are derived from a ferritin heavy chain locus.
- 5. A genetic vector as in any one of claims 1-2 wherein said proximal 5' regulatory sequences and said distal 5' flanking sequences are derived from a ferritin heavy chain locus.
 - 6. A genetic vector as in any one of claims 1-5 wherein said proximal 3' regulatory sequences are derived from a ferritin heavy chain locus.
 - 7. A genetic vector as in any one of claims 1-6 further comprising distal 3' flanking sequences of a ferritin heavy chain locus.
- 8. A genetic vector as in any one of claims 1, and 3-7 wherein said insertion site
 25 for a heterologous sequence includes at least one restriction endonuclease site.
 - 9. A genetic vector as in claim 8 wherein said insertion site for a heterologous sequence is a polylinker site including at least two restriction endonuclease sites.
- 30 10. A genetic vector as in any one of claims 1-9 wherein said proximal 5' regulatory sequences include a eukaryotic intron sequence.





- 12. A genetic vector as in any one of claims 1-11 wherein said proximal 5'
 5 regulatory sequences include untranslated exon sequences.
 - 13. A genetic vector as in any one of claims 1-12 wherein said distal 5' flanking sequences and said proximal 5' regulatory sequences have a total length of between 1,000 and 10,000 bases.

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- 14. A genetic vector as in any one of claims 1-12 wherein said proximal 3' regulatory sequences and any distal 3' flanking sequences have a total length of between 1,000 and 10,000 bases.
- 15 15. A eukaryotic cell transfected with a vector of any one of claims 1-14.
 - 16. A eukaryotic cell as in claim 15 wherein said vector has stably integrated into a chromosome of said cell.
- 20 17. A eukaryotic cell as in any one of claims 15-16 wherein said first coding sequence is expressed in said cell.
 - 18. A eukaryotic cell comprising
 - (a) distal 5' flanking sequences of a eukaryotic locus;
- 25 (b) proximal 5' regulatory sequences of a eukaryotic locus;
 - (c) at least a first coding sequence; and
 - (d) proximal 3' regulatory sequences effective for transcription termination of a eukaryotic locus;

wherein said sequences are operably joined in order (a)-(d) in a 5' to 3' orientation, with optional linker sequences between adjacent sequences; and wherein



- (1) said distal 5' flanking sequences comprise an exogenous sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus; or
- (2) said proximal 5' regulatory sequences comprise an exogenous sequence of at least 20 bases having at least 70% identity to a nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.
- 19. A eukaryotic cell comprising:
 an exogenous 5' distal flanking sequence derived from a ferritin heavy chain
 10 locus operably joined to a coding sequence.
 - 20. A method of producing a desired protein in a eukaryotic cell comprising:
 - (a) providing at least one cell of any one of claims 15-19 or a descendent thereof;
- 15 (b) maintaining said cell in a culture under conditions which permit high expression of said desired protein; and
 - (c) isolating said desired protein from said culture.